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OM nucleic - nucleic search, using sw model

Run on: October 13, 1999, 14:43:47 : Search time 2579.19 seconds  
(without alignments)  
11986.627 Million cell updates/sec

Title: US-09-247-874-2  
Perfect score: 9721  
Sequence: 1 agaaagaagagagagagaa.....ccgttgacctgcagctgcac 9721

Scoring table: IDENTIT\_NUC

Searched: 679419 segs, 1590154680 residues

base :

GenEmbl: \*  
1: gb\_ba1.\*  
2: gb\_ba2.\*  
3: gb\_em.\*  
4: gb\_ov.\*  
5: gb\_pat.\*  
6: gb\_ph.\*  
7: gb\_pl1.\*  
8: gb\_pl2.\*  
9: gb\_pl3.\*  
10: gb\_pl4.\*  
11: gb\_pl5.\*  
12: gb\_pl6.\*  
13: gb\_pl7.\*  
14: gb\_pl8.\*  
15: gb\_pl9.\*  
16: gb\_pl10.\*  
17: gb\_pl11.\*  
18: gb\_pl12.\*  
19: gb\_pl13.\*  
20: gb\_pl14.\*  
21: gb\_pl15.\*  
22: gb\_pl16.\*  
23: gb\_pl17.\*  
24: gb\_pl18.\*  
25: gb\_pl19.\*  
26: gb\_pl20.\*  
27: gb\_pl21.\*  
28: gb\_pl22.\*  
29: gb\_pl23.\*  
30: gb\_pl24.\*  
31: gb\_pl25.\*  
32: gb\_pl26.\*  
33: gb\_pl27.\*  
34: gb\_pl28.\*  
35: gb\_pl29.\*  
36: gb\_pl30.\*  
37: gb\_pl31.\*  
38: gb\_pl32.\*  
39: gb\_pl33.\*  
40: gb\_pl34.\*  
41: gb\_pl35.\*  
42: gb\_pl36.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	9717.4	100.0	9721	10	HSILB	X04500 Human gene

2	7208.8	74.2	7824	9	HOMILB	M15840 Human inter
3	1688.2	17.4	1773	5	A01613	A01613 DNA sequenc
4	1107.4	11.4	8760	3	SSPINTB	X74568 S. scrofa ge
5	807.6	8.3	1472	10	HSPROIB	X56087 Human mRNA
6	807.4	8.3	1497	5	E08734	E08734 DNA encodi
7	788.6	8.1	1507	5	E00846	M15330 Human inter
8	788.6	8.1	1507	5	E07942	E00846 DNA sequen
9	780.8	8.0	1496	9	HUMIL1	I07942 Sequence 1
10	769.8	7.9	1514	5	I00729	I00729 Human monoc
11	766.8	7.9	1496	9	HOMILIC	M54933 Human monoc
12	764.8	7.9	1404	5	A21148	A21148 p61f- alpha
13	764.8	7.9	1404	5	E01230	E01230 DNA encodi
14	764.8	7.9	1404	26	E11934	E11934 CDNA encodi
15	764.8	7.9	1404	26	E12090	E12090 Human cDNA
16	764.4	7.9	1404	5	I00228	I00228 Sequence 2
17	764.4	7.9	1404	5	I01156	I01156 Sequence 1
18	756.4	7.8	1459	5	E02498	E02498 CDNA encodi
19	637.2	6.6	1458	5	E02498	E02498 CDNA encodi
20	612.4	6.3	614	14	G10509	G10509 human SFS C
21	573.2	5.9	7100	12	NMILIB	X04964 Murine inte
22	553	5.7	553	10	HSPROINB	X52430 H. sapiens D
23	457.6	4.7	1124	10	HSILIB	X02532 Human mRNA
24	445.6	4.6	1125	5	E00619	E00619 CDNA encodi
25	423.2	4.4	776	15	SYNLIBA	M15534 Synthetic h
26	400	4.1	400	14	G13631	G13631 Human SFS S
27	395	4.1	395	10	HSPROINS7	X52431 H. sapiens D
28	379.6	3.9	1473	3	EC92481	U92481 Equus cabal
29	360	3.7	1458	3	P16PILKNB	M86725 Sus scrofa
30	331.4	3.4	594	5	E01445	E01445 Decombinant
31	331.2	3.4	1429	5	A19155	A19155 ovine IL-1
32	325.8	3.4	1895	3	AF026543	AF026543 Bos tauru
33	307.4	3.2	1895	5	E01591	E01591 CDNA encodi
34	293.4	3.0	1736	3	BOVILIB	M37211 Bovine inte
35	293.4	3.0	1736	3	BOVILIB	M37211 Bovine inte
36	260.6	2.7	502	11	AF043335	AF043335 Homo sapi
37	251.2	2.6	141851	10	HSB75N13	Z82216 Human DNA s
38	250.2	2.6	143748	10	HSB75N13	Z82216 Human DNA s
39	250.2	2.6	136298	34	HS796117	AL033398 Homo sapi
40	249.4	2.6	133060	42	AC006474	AC006474 Homo sapi
41	249.4	2.6	162556	42	AC006017	AC006017 Homo sapi
42	249.2	2.6	131070	11	AC005295	AC005295 Homo sapi
43	248	2.6	149554	10	HSAC000111	AC000111 Human BAC
44	248	2.6	1437	12	AF119622	AF119622 Cavia por
45	247.6	2.5	130988	9	HS364122	AL031012 Human DNA

## ALIGNMENTS

RESULT	1	HSILB	9721 bp	DNA	PRI	26-JUN-1997
LOCUS	HSILB					
DEFINITION	Human gene for prointerleukin 1 beta.					
ACCESSION	X04500					
NID	933788					
VERSION	X04500.1					
KEYWORDS	interleukin 1 beta.					
SOURCE	human.					
ORGANISM	Homo sapiens					

REFERENCE  
1 (bases 1 to 9721)  
Clark, B.D., Collins, K.L., Gandy, M.S., Webb, A.C. and Aueron, P.E.

TITLE  
Genomic sequence for human prointerleukin 1 beta: possible evolution from a reverse transcribed prointerleukin 1 alpha gene

JOURNAL  
Nucleic Acids Res. 14 (20), 7897-7914 (1986)

MEDLINE  
87040762  
Erratum: [[published erratum appears in Nucleic Acids Res 1987 Jan 26;15(2):868]]

COMMENT  
Data kindly reviewed (13-MAY-1988) by Clark B.D.  
FEATURES  
Location/Qualifiers  
1..9721  
/organism="Homo sapiens"



QY	1861	aacgagaaatttcagcctctactctcgtcttggaaagctataaacaacgagga	1920
Db	1861	AACGAGAAATTTCAGCCTCTACTCTCGCTTTGAAAGCTATAAAGCGAAGGA	1920
QY	1921	gaactgcgaatcccaacctcttcgagcgacaagcgacaacagctcctcgtgattc	1980
Db	1921	GAACCTGCGAATCCCAACCTCTTCGAGCGACAAGCGACAAGGCTCTCTGGATTCC	1980
QY	1981	tcttcagccaattctcatctgctcaaglatgaacttaattctctctacaactagatgctaa	2040
Db	1981	TCTTCAGCCAATTCCTATCTGCTCAGATGATGACTTTATCTCTCTTCACACTAGGTGCTAA	2040
QY	2041	gggagctctctctgctctctcgtcctcttggtagtgcatactctctctctctct	2100
Db	2041	GGGAGCTCTCTCTGCTCTCTCGCCTTTGGTGTATGCAATATCTCTCTCTCTCT	2100
QY	2101	tcttcctctgctctctctctctctctctctctctctctctctcagccttcggcaaaag	2160
Db	2101	TCTTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAGCTTTTGGCAAAAATG	2160
QY	2161	ccaggctgcaataatgctattagctcgcgggaaaattctcggaaatgaaactgctatct	2220
Db	2161	CGAGGTGAATATATAGTTATGACTGCGGAATATCTTGGAAATGATAGCTATATCT	2220
QY	2221	aacagctgaacccctaaaggttagtgcgaagcctctgcacagctctccctagccaatc	2280
Db	2221	AACAGCTGACCCCTAAAGGTTAGTGCGAAGCCTCTGCTCCAGCTCTCTTAGCCAAATAC	2280
QY	2281	attgtagttgggtttgggttagcaatgctttctcagaccgaagaactctctctt	2340
Db	2281	ATTGTTAGTTGGGTGGGTGGTTTACCAATCTTTCTCTAGACCAAGGACTCTCTTT	2340
QY	2341	caacatctcatctattactcagaagatcaattctcttgactgcgaactgagatgc	2400
Db	2341	CACATCTCATCTATTACTCAGAGATCAATTTCTTGCAAGACTGCACAGACTGGATGC	2400
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Db	2401	TGAGGAATCCACACTGAATGAAGTGGCGGTATGGGGAAGCACTCAATTTCTCTTTTA	2460
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Db	2461	CACAGGTCTCGAAGCACATGACAAAGTACGACAAAGTACTGAGCTCGCCAGTAAATGATGGCTT	2520
QY	2521	attacaagctcagctgagagacgctcagacaagaatacagaatcaggtctctctctcaagat	2580
Db	2521	ATTAAAGCTCAGCTGAGAGCGCTGAGACCAAGTAAATAGCAGGCTCTCTTTCAAGAT	2580
QY	2581	agagtgatactgctgcttgagaccagaatttctccctaattgctcctcttcaggtaa	2640
Db	2581	AGAGTGATATCTGCTCTTGAGACCAAGTATTTCCCTAAATGGCTCTCTTAGTGGCAA	2640
QY	2641	acaaggtgcgaagtcataatctgatttaaagactacttctccatacaagttccctccagct	2700
Db	2641	ACAGGTTGCAAGTAAATCTATTTAAAGACTACTTTCCATTTACAAGTCCCTCCAGCT	2700
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QY	2761	agaaaaagatctcaagcaccacaatacaagaatccctctgcaaatgctgagcttgaaaggag	2820
Db	2761	AGAAAAAGATCTCCAAACCCACAAATACAAAGGAATCCCTTTGCAAAAGTGGCTTGAGAGGAG	2820
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Db	2821	AGGAGAGAGCTCAGATTTTAGCTGACTCTGCTGGGCTTAGAGGTTAGGCTCAAAATCCAAC	2880
QY	2881	aggagagaccaaaggtgacacactcacaagccttagaatctcctctgagctgtctcgag	2940
Db	2881	AGGAGACCAAGGCTGACCACTCTCCAGGCTAATAATCTGCTTCTGAGCTGTCTTGCGC	2940



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 Db 5161 GCGGCAATCCAGCTACGAATCTCCGACACCACTACAGCAAGGCGCTTCAGGCGCGG 5220  
 QY 5221 tcaattgtgtgcatcagcaagctgaggaagatgctgttcctccgccaagaccttc 5280  
 Db 5221 TCAGTTGTGTGGCCATGACAGAGCTAGAGAAATCTGTGTTCCCTCCACAGACTTC 5280  
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9481 aatccagcacttgggtgaggggagagagatgctgtgacccagaggttcaagacc 9540

